

G1 position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, and G475 in *Bacillus licheniformis* (SEQ ID NO:2).

G2 118. (Amended.) The alpha-amylase according to claim 113, wherein said alpha- amylase further comprises a substitution or deletion at one or more residues equivalent to A209 and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

G3 126. (Amended.) The alpha-amylase according to claim 121, wherein said alpha-amylase further comprises a substitution or deletion at one or more residues equivalent to A209 and/or M197.

G4 193. (Amended.) A variant of a parent alpha-amylase, said variant having an amino acid sequence which differs from the amino acid sequence of said parent, wherein the difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at one or more positions selected from the group consisting of the positions which correspond to amino acid residues Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, G433, and G475 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2); wherein said variant has alpha-amylase activity.

G5 194. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue Q298 in *Bacillus licheniformis* alpha-amylase.

GF 195. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G299 in *Bacillus licheniformis* alpha-amylase.

196. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G301 in *Bacillus licheniformis* alpha-amylase.

197. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue Y302 in *Bacillus licheniformis* alpha-amylase.

198. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue L307 in *Bacillus licheniformis* alpha-amylase.

199. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue F343 in *Bacillus licheniformis* alpha-amylase.

200. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue F403 in *Bacillus licheniformis* alpha-amylase.

65 201. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue H405 in *Bacillus licheniformis* alpha-amylase.

202. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue H406 in *Bacillus licheniformis* alpha-amylase.

203. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue D407 in *Bacillus licheniformis* alpha-amylase.

204. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G427 in *Bacillus licheniformis* alpha-amylase.

205. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue I428 in *Bacillus licheniformis* alpha-amylase.

206. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue D430 in *Bacillus licheniformis* alpha-amylase.

G5 207. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G433 in *Bacillus licheniformis* alpha-amylase.

208. (Amended.) The variant according to claim 193, wherein said difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G475 in *Bacillus licheniformis* alpha-amylase.

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G6 213. (Amended.) A variant of a parent alpha-amylase, said variant having an amino acid sequence which differs from the amino acid sequence of said parent, wherein the difference between said variant and said parent consists of a different amino acid residue in said variant than in said parent at one or more positions selected from the group consisting of the positions which correspond to amino acid residues Q298, G299, G301, Y302, L307, H405, H406, D407, I428, D430, and G475 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2); wherein said variant has alpha-amylase activity.

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